RAW SEQUENCE LISTING PATENT APPLICATION US/08/804,166

DATE: 04/10/97 TIME: 08:46:56

INPUT SET: S16859.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

1		SEQUENCE LISTING
2		C_{α} D_{α}
3	(1) Ge	SEQUENCE LISTING eneral Information: APPLICANT: Campbell, Robert K. Jameson, Bradford A. Chappel, Scott C. TITLE OF INVENTION: HYBRID PROTEINS
4		COO NOT CO
5	(1)	APPLICANT: Campbell, Robert K.
6		Jameson, Bradford A.
7 8		Chappel, Scott C.
9	/ 1 1 1	TITLE OF INVENTION: HYBRID PROTEINS
10	(11)	TITLE OF INVENTION. HIBRID PROTEINS
11	(iii)	NUMBER OF SEQUENCES: 22
12	(/	
13	(iv)	CORRESPONDENCE ADDRESS:
14	, ,	(A) ADDRESSEE: BROWDY AND NEIMARK
15		(B) STREET: 419 Seventh Street N.W., Ste. 300
16		(C) CITY: Washington
17		(D) STATE: D.C.
18		(E) COUNTRY: USA
19		(F) ZIP: 22207
20		
21	(V)	COMPUTER READABLE FORM:
22		(A) MEDIUM TYPE: Floppy disk
23		(B) COMPUTER: IBM PC compatible
24		(C) OPERATING SYSTEM: PC-DOS/MS-DOS
25		(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26	مستر (۱۰۰۰)	(B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: Patentin Release #1.0, Version #1.30 PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 60/011,936 (B) FILING DATE: 20 February 1996 (C) CLASSIFICATION:
27	$(\Lambda^{(l)})$	PRIOR APPLICATION DATA:
28 29		(A) APPLICATION NUMBER: 60/011,936
30		(B) FILING DATE: 20 February 1996 (C) CLASSIFICATION:
31		(C) CLASSIFICATION:
32	(viii)	ATTORNEY/AGENT INFORMATION:
33	(• = = =)	(A) NAME: Browdy, Roger L.
34		(B) REGISTRATION NUMBER: 25,618
35		(C) REFERENCE/DOCKET NUMBER: CAMPBELL=2A
36		
37	(ix)	TELECOMMUNICATION INFORMATION:
38	• • •	(A) TELEPHONE: (202) 628-5197
39		(B) TELEFAX: (202) 737-3528
40		•
41	(2) INFOR	MATION FOR SEQ ID NO:1:
42		
43	(i)	SEQUENCE CHARACTERISTICS:
44		(A) LENGTH: 1049 base pairs
45		(B) TYPE: nucleic acid
46		(C) STRANDEDNESS: single

RAW SEQUENCE LISTING PATENT APPLICATION US/08/804,166

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48	((ii)	MOI	LECUI	LE T	PE:	CDN	A									
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50	((ix)		ATURI													
51			-	A) NA													
52			(I	3) L(CAT:	CON:	278	104	17								
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54	((Xi)	SE	QUEN	CE DI	ESCR.	[PTIC	ON: S	SEQ :	ID NO	0:1:						
55																	
56	TCCAC	CATG	igc !	racac	GT'A	AG CO	3CCC(CTAA	A ATO	CCCT"	rtgg	GCA	CAAT	GTG '	rccre	BAGGGG	60
57								,,,,,,		~m.s.s.		a. a.			3.00m		100
58	AGAGG	CAG	icg A	ACCTO	J'I'AG <i>I</i>	AT GO	3GAC(3GGG(3 CA	CTAAC	CCT	CAG	3TTTT	JGG (3CTTC	CTCAAT	120
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60 61	CTCAC	TAT	CG (CAT	JAA	sc cc	AGT	1111	انان و	JAAT	JICA	GAAA	AGCT	JCT (CIC	CIGGA	180
62	CCCAT	מממ	C2 (7202		י א די		ישממי	ת ממי		יממא	מאמי	פרכיים	700 (יוויטווים	rgctct	240
63	GGGAI	GGA	IGA (JAGAI	MMM	-A A1	ACAG	100		HUCH	JUGA	GAG.	IGCI	366 (.101	IGCICI	240
64	CCGGC	ייייטריי	יכיים נ	مشكشا	רמכים <i>ו</i>	יות כוו	וממשי	ኮጥረነጥረ	י ממנ	י אממני	T TPC/	י רפי	2 100	3 ጥርረ	י מייני	ב כיזיכי	295
65	CCGGC	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		.101	GCC		I GG I .	11010		CAGG						ı Leu	275
66												l Ari	,			5	
67												_			•	•	
68	CTG G	CT	ттт	GGC	CTG	СТС	TGC	CTG	CCC	TGG	СТТ	CAA	GAG	GGC	AGT	GCC	343
69	Leu A																
70				10			2		15	•	_			20			
71																	
72	GAT A	AGT	GTG	TGT	CCC	CAA	GGA	AAA	TAT	ATC	CAC	CCT	CAA	AAT	AAT	TCC	391
73	Asp S	Ser	Val	Cys	Pro	Gln	Gly	Lys	Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	
74	_		25	_			_	30	_				35				
75																	
76	ATT T	ľGC	TGT	ACC	AAG	TGC	CAC	AAA	GGA	ACC	TAC	TTG	TAC	AAT	GAC	TGT	439
77	Ile C	'ys	Cys	Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	
78		40					45					50					
79																	
80	CCA G																487
81	Pro G	31y	Pro	Gly	Gln		Thr	Asp	Cys	Arg		Cys	Glu	Ser	GTÀ		
82	55					60					65					70	
83			aam	ma.	a.,		~~~	ama		a.a	maa	ama		maa	maa		E 3 E
84	TTC A																535
85 86	Phe T	ınr	Ата	ser		ASN	HIS	Leu	Arg		cys	Leu	Ser	cys		ràs	
87					75					80					85		
88	TGC C	ימא	ΔAG	GNA	ΔͲΟ	GGT	CAG	GTG.	GAG	ΔͲሮ	ጥርጥ	ጥርጥ	ጥርረ	ACA	GTG	GAC	583
89	Cys A																303
90	Cys A	·- 9	-73	90		OLY.			95			201	~ J S	100	*41		
91				70					,,								
92	CGG G	AC	ACC	GTG	TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	ТАТ	TGG	631
93	Arg A																
94			105		- 1 -		- 1 -	110	-1-			- 4 -	115		- 4 -		
95	•																
96	: AGT G	AA	AAC	CTT	TTC	CAG	TGC	TTC	AAT	TGC	AGC	CTC	TGC	CTC	AAT	GGG	679
97	Ser G																
98	-	20					125			_		130	-			-	
99																	

RAW SEQUENCE LISTING PATENT APPLICATION US/08/804,166

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100	ACC	GTG	CAC	CTC	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG	TGC	ACC	TGC	727
101				Leu													
102	135					140			-		145					150	
103																	
104	CAT	GCA	GGT	TTC	TTT	CTA	AGA	GAA	AAC	GAG	TGT	GTC	TCC	TGT	GCC	GGT	775
105	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu	Cys	Val	Ser	Cys	Ala	Gly	
106			_		155		_			160	_				165		
107																	
108	GCT	GCC	CCA	GGT	TGC	CCA	GAA	TGC	ACG	CTA	CAG	GAA	AAC	CCA	TTC	TTC	823
109	Ala	Ala	Pro	Gly	Cys	Pro	Glu	Cys	Thr	Leu	Gln	Glu	Asn	Pro	Phe	Phe	
110				170	_			-	175					180			
111																	
112	TCC	CAG	CCG	GGT	GCC	CCA	ATA	CTT	CAG	TGC	ATG	GGC	TGC	TGC	TTC	TCT	871
113	Ser	Gln	Pro	Gly	Ala	Pro	Ile	Leu	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser	
114			185					190					195				
115																	
116	AGA	GCA	TAT	CCC	ACT	CCA	CTA	AGG	TCC	AAG	AAG	ACG	ATG	TTG	GTC	CAA	919
117	Arg	Ala	Tyr	Pro	Thr	Pro	Leu	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Gln	
118		200					205					210					
119																	
120	AAG	AAC	GTC	ACC	TCA	GAG	TCC	ACT	TGC	TGT	GTA	GCT	AAA	TCA	TAT	AAC	967
121	Lys	Asn	Val	Thr	Ser	Glu	Ser	Thr	Cys	Cys	Val	Ala	Lys	Ser	Tyr	Asn	
122	215					220					225					230	
123																	
124				GTC													1015
125	Arg	Val	Thr	Val	Met	Gly	Gly	Phe	Lys		Glu	Asn	His	Thr	Gly	Cys	•
126					235					240					245		
127																	
128				ACT							TA	AG					1049
129	His	Cys	Ser	Thr	Cys	Tyr	Tyr	His	_	Ser							
130				250					255								
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137		1	(1) :	SEQUE							_						
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147 148	T				3			_		10					13		
148	T corr	a1 ~	gl.,	Gly	202	λ T =) en	Ser	Val	Cve	Dro	G] n	G1 17	T.ve	ጥ፣ታ	Tla	
150	Leu	GIII	GIU	20	261	WIG	wah	- 261	25	Cys	FIU	GIII	GTA	30 Lys	TAT	116	
151				20			1	•	د يد.					30			
101			_				_			_							

152 His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr

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154	153			35					40					45	II	PUI	SEI:
156		m	-	m	•	•	a	D	a1	D	a1	a1	>	m\	•	a	3
157		Tyr		Tyr	Asn	Asp	cys		стЪ	Pro	GTÀ	GIN		Thr	ASP	cys	Arg
158			50					33					00				
159		Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His
161	159		-			-										_	
162											_		_	_		_	_
Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn 100		Cys	Leu	Ser	Cys		Lys	Cys	Arg	Lys		Met	Gly	Gln	Val		Ile
164 Ser Ser Cys Thr Val Asp Asp Thr Val Cys Gly Cys Arg Lys Asn 106 106 107 Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys 125 126 127 128 129 125 120 125						85					90					95	
165		Ser	Ser	Cvs	Thr	Val	Asp	Ara	Asp	Thr	Val	Cvs	Glv	Cvs	Ara	Lvs	Asn
166		501	501	O J D			пор	9	тор		,,,	4	0_1	0,0	_	_,_	
168																	
169		Gln	Tyr	Arg	His	Tyr	Trp	Ser		Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys
170				115					120					125			
171				a	T		~ 1	mla		***	T	~~		a 1	a1	T	a 1 =
172		Ser		cys	Leu	ASN	СТА		vaı	HIS	Leu	ser	_	GIN	GIU	гÀг	GIN
173			130					133					140				
175 176 177 176 178 179 179 179 180 180 180 180 180 180 180 180 180 180		Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu	Asn	Glu
176	174	145			_		150			_		155		_			160
177			_			_	_	_	_					_			
178 179		Cys	Val	Ser	Cys		Gly	Ala	Ala	Pro	-	Cys	Pro	Glu	Cys		Leu
179 Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys 180 180 185 190 190 181 182 Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys 183 195 200 205 20						165					170					1/5	
180		Gln	Glu	Δsn	Pro	Phe	Phe	Ser	Gln	Pro	G] v	Δla	Pro	Tle	T.eu	Gln	Cvs
181 182 Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys 183 195 200 205 184 185 Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys 186 210 215 220 187 188 Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val 189 225 230 235 240 190 191 Glu Asn His Thr Gly Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser 192 245 255 193 194 195 (2) INFORMATION FOR SEQ ID NO:3: 196 197 (i) SEQUENCE CHARACTERISTICS: 198 (A) LENGTH: 1202 base pairs 199 (B) Type: nueleic acid 200 (C) STRANDEDNESS: single 201 (D) TOPOLOGY: linear 202 203 (ii) MOLECULE, Type: cDNA		GIII	GIU	ASII		1116	£ 11C	Der	0111		OL y	ALU	110	***		O1	O J D
183																	
184 185 Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys 186 210	182	Met	Gly	Cys	Cys	Phe	Ser	Arg	Ala	Tyr	Pro	Thr	Pro	Leu	Arg	Ser	Lys
Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys 210				195					200					205			
186		•					~ 7	-	•	••- •	m1	~	a 1	~	m\	~	~
187 188 Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val 189 225		гàг		мет	Leu	vaı	GIN		ASN	vaı	Thr	ser		ser	Thr	cys	cys
188 Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val 189 225 230 235 240 240			210					215					220				
189 225 230 235 240 190 191 Glu Asn His Thr Gly Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser 192 245 250 255 193 194 195 (2) INFORMATION FOR SEQ ID NO:3: 196 197 (i) SEQUENCE CHARACTERISTICS: 198 (A) LENGTH: 1202 base pairs 199 (B) TYPE: nueleic acid 200 (C) STRANDEDNESS: single 201 (D) TOPOLOGY: linear 202 203 (ii) MOLECULE TYPE: cDNA 204		Val	Ala	Lys	Ser	Tyr	Asn	Arg	Val	Thr	Val	Met	Gly	Gly	Phe	Lys	Val
Glu Asn His Thr Gly Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser 192 245 250 255 193 194 195 (2) INFORMATION FOR SEQ ID NO:3: 196 197 (i) SEQUENCE CHARACTERISTICS: 198 (A) LENGTH: 1202 base pairs 199 (B) TYPE: nueleic acid 200 (C) STRANDEDNESS: single 201 (D) TOPOLOGY: linear 202 203 (ii) MOLECULE TYPE: cDNA 204	189			-		-		•					_	_		_	
192																	
193 194 195 (2) INFORMATION FOR SEQ ID NO:3: 196 197 (i) SEQUENCE CHARACTERISTICS: 198 (A) LENGTH: 1202 base pairs 199 (B) TYPE: nueleic acid 200 (C) STRANDEDNESS: single 201 (D) TOPOLOGY: linear 202 203 (ii) MOLECULE TYPE: cDNA		Glu	Asn	His	Thr		Cys	His	Cys	Ser		Cys	Tyr	Tyr	His		Ser
194 195 (2) INFORMATION FOR SEQ ID NO:3: 196 197 (i) SEQUENCE CHARACTERISTICS: 198 (A) LENGTH: 1202 base pairs 199 (B) TYPE: nueleic acid 200 (C) STRANDEDNESS: single 201 (D) TOPOLOGY: linear 202 203 (ii) MOLECULE TYPE: cDNA 204						245					250					255	
195 (2) INFORMATION FOR SEQ ID NO:3: 196 197 (i) SEQUENCE CHARACTERISTICS: 198 (A) LENGTH: 1202 base pairs 199 (B) TYPE: nueleic acid 200 (C) STRANDEDNESS: single 201 (D) TOPOLOGY: linear 202 203 (ii) MOLECULE TYPE: cDNA 204																	
196 197 (i) SEQUENCE CHARACTERISTICS: 198 (A) LENGTH: 1202 base pairs 199 (B) TYPE: nueleic acid 200 (C) STRANDEDNESS: single 201 (D) TOPOLOGY: linear 202 203 (ii) MOLECULE TYPE: cDNA 204		(2)	TNF	רבאאר	PTON	FOR	SEO	ז מד	VO : 3 :	2							
197 (i) SEQUENCE CHARACTERISTICS: 198 (A) LENGTH: 1202 base pairs 199 (B) TYPE: nueleic acid 200 (C) STRANDEDNESS: single 201 (D) TOPOLOGY: linear 202 203 (ii) MOLECULE TYPE: cDNA 204		(2)		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		- 010	226			,							
199 (B) TYPE: nueleic acid 200 (C) STRANDEDNESS: single 201 (D) TOPOLOGY: linear 202 203 (ii) MOLECULE TYPE: cDNA 204			(i)	SE	QUENC	CE CH	IARAC	CTER	STI	cs:							
200 (C) STRANDEDNESS: single 201 (D) TOPOLOGY: linear 202 203 (ii) MOLECULE TYPE: cDNA 204	198		•								cs						
201 (D) TOPOLOGY: linear 202 203 (ii) MOLECULE TYPE: cDNA 204																	
202 203 (ii) MOLECULE TYPE: cDNA 204										gle							
203 (ii) MOLECULE TYPE: cDNA 204				(1	ד (ע	J r⊕ L(JGY:	Tine	ear								
204			/ i i '	MOT	ינוטים	. ው. ጥነ	DF.	CDN	۸.								
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			(ix)) FE	ATURE	፤ :											

RAW SEQUENCE LISTING PATENT APPLICATION US/08/804,166

DATE: 04/10/97 TIME: 08:47:05

														II	VPUI	SE1: S10	osy.raw
206			•	A) NA				• • •	••								
207 208			(1	B) L(JCAT.	TON:	279	•• • • • •	99								
208		/vi	SE(QUENC	e Di	ESCR.	ΓΡΨΤ)N: 9	SEO '	TD NO):3:						
210		(AT	, 55,	SODW.	, D	BOCK.		J14	JUY .								
211	CTC	BAGA!	rgg (CTAC	AGGT	AA G	CGCC	CCTA	A AA'	rccc:	TTTG	GGC	ACAA'	rgt (GTCC:	rgaggg	60
212																	
213	GAG	AGGT	AGC (GACC!	rgta(GA TO	GGA (CGGG	G GC	ACTA	ACCC	TGA	GTT'	rgg (GCT.	CTGAA	120
214																	
215	TGT	BAGT	ATC (GCCA!	rgta.	AG C	CCAG!	ratt'	r gg	CCAA	rgtc	AGA	AAGC'	rcc '	rggt	CCCTGG	180
216	3.00	3 B M C /						aamaa	- ma	3300		3034	amaai	naa <i>i</i>	aamar	BMCGMG	240
217 218	AGGG	3A'I'G(SAG A	AGAGA	AAAA	AC A	AACAG	3CTC(TG	JAGC	AGGG	AGA	3TGC	rgg (JCTC.	PTGCTC	240
219	TCCC	GCT(ימם י	гстст	PTGC	C TO	зтааг	րդուն	г сс	CCAGO	зс то	ad de	G A	CG TO	cc c	rg	293
220	1000	30011													er Le		2,0
221													<i>J</i>		50		
222																	
223															GGC		341
224	Leu	Leu	Ala		Gly	Leu	Leu	Cys		Pro	Trp	Leu	Gln		Gly	Ser	
225				265					270					275			
226 227	000	C a m	N CITT	ama	mam	000	CA A	003		mam	N TO CO	axa	a a m	C1 X X	AAT	2 2 17	389
227															Asn		309
229	ALU	ASP	280	V U L	Cyb	110	01	285	Lys	.,.		****	290	41			
230																	
231	TCG	ATT	TGC	TGT	ACC	AAG	TGC	CAC	AAA	GGA	ACC	TAC	TTG	TAC	AAT	GAC	437
232	Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	
233		295					300					305					
234		~~>		~~~	-	a. a	a.m		a.a	maa		a.a	mam	a. a	100	000	405
235 236															AGC Ser		485
236	310	PIO	сту	PIO	сту	315	ASD	1111	АЗР	Cys	320	GIU	cys	GIU	261	325	
238	310					010					520					020	
239	TCT	TTC	ACC	GCT	TCA	GAA	AAC	CAC	CTC	AGA	CAC	TGC	CTC	AGC	TGC	TCC	533
240	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys	Ser	
241					330					335					340		
242																	
243															ACA		581
244 245	гÀг	cys	arg	Lys 345	GIU	мет	GTA	GIN	350	GIU	тте	ser	Ser	355	Thr	vaı	
245				343					330					333			
247	GAC	CGG	GAC	ACC	GTG	TGT	GGC	TGC	AGG	AAG	AAC	CAG	TAC	CGG	CAT	TAT	629
248															His		
249	-	-	360			-	_	365	_				370	_		_	
250																	
251															CTC		677
252	Trp		Glu	Asn	Leu	Phe		Cys	Phe	Asn	Cys		Leu	Cys	Leu	Asn	
253 254		375		_			380					385					
254 255	GGG	ልሮሮ	GTG	CAC	ርጥሮ	TCC	ጥሮሮ	CAG	GAG	ΔΔΔ	CAG	אאר	ACC	GTG	TGC	ACC	725
256															Cys		, 23
257	390			J		395	- 1 -			_1_	400				4 ~	405	
258																	

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/08/804,166

DATE: 04/10/97 TIME: 08:47:08

INPUT SET: S16859.raw

APPLICATION NUMBER FILING DATE CLASSIFICATION CURRENT APPLICATION DATA

Observed my	<u>/66</u>	CRF Processing Date: 4/10/01/01/01/01/01/01/01/01/01/01/01/01/
Changed a file from nor	n-ASCII to ASCII	Verified by:(ST
Changed the margins in	n cases where the sequence text	was "wrapped" down to the next line.
Edited a format error in	the Current Application Data sec	ction, specifically:
	ication Data section with the acturation application data; or other	ual current number. The number inputted by
Added the mandatory h	eading and subheadings for "Cu	rrent Application Data".
Edited the "Number of S	Sequences" field. The applicant	spelled out a number instead of using an integ
Changed the spelling of	a mandatory field (the headings	or subheadings), specifically:
Corrected the SEQ ID N	IO when obviously incorrect. The	e sequence numbers that were edited were:
nserted or corrected a r	nucleic number at the end of a nu	, ucleic line. SEQ ID NO's edited:
- •	•	e on the same line as each subheading. If the was moved to its appropriate place.
Inserted colons after he	eadings/subheadings. Headings	and the section of a section of the
inserted colons after he	adings subheadings. Treadings	edited included:
	eadings used by an applicant, sp	
Deleted extra, invalid, h	readings used by an applicant, sp	oecifically: of files; secretary initials/filename at end
Deleted extra, invalid, h Deleted: non-ASCII page numbers thro	eadings used by an applicant, sports of the deginning/end bughout text; other invalid texts	of files; secretary initials/filename at end
Deleted extra, invalid, h Deleted: non-ASCII page numbers thro Inserted mandatory hea	eadings used by an applicant, sports of the deginning/end bughout text; other invalid texts	oecifically: of files; secretary initials/filename at end xt, such as
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Deleted extra, invalid, h Deleted: non-ASCII page numbers thro Inserted mandatory hea Corrected an obvious e	l "garbage" at the beginning/end bughout text; other invalid textaddings, specifically:	of files; secretary initials/filename at end at, such as see is required, or vice versa.
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*Examiner: The above corrections must be communicated to the applicant in the first Office 3/1/95 Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING PATENT APPLICATION US/08/804,166

DATE: 04/10/97 TIME: 17:05:27

INPUT SET: S16859.raw

This Raw Listing contains the General Information Section and up to the first, 5 pages.

```
WERED
                                       SEQUENCE LISTING
 1
 2
 3
           General Information:
    (1)
 4
 5
          (i) APPLICANT: Campbell, Robert K.
 6
                         Jameson, Bradford A.
 7
                         Chappel, Scott C.
 8
        (ii) TITLE OF INVENTION: HYBRID PROTEINS
 9
10
       (iii) NUMBER OF SEQUENCES: 22
11
12
        (iv) CORRESPONDENCE ADDRESS:
13
14
               (A) ADDRESSEE: BROWDY AND NEIMARK
               (B) STREET: 419 Seventh Street N.W., Ste. 300
15
16
               (C) CITY: Washington
17
               (D) STATE: D.C.
               (E) COUNTRY: USA
18
19
               (F) ZIP: 22207
20
          (V) COMPUTER READABLE FORM:
21
22
               (A) MEDIUM TYPE: Floppy disk
23
               (B) COMPUTER: IBM PC compatible
24
               (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25
               (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27
       (vi)
             CURRENT APPLICATION DATA:
28
               (A) APPLICATION NUMBER:
29
               (B) FILING DATE:
30
               (C) CLASSIFICATION:
31
       (vii) PRIOR APPLICATION DATA:
32
33
               (A) APPLICATION NUMBER:
                                         60/011,936
34
               (B) FILING DATE: 20 February 1996
35
               (C) CLASSIFICATION:
36
      (viii) ATTORNEY/AGENT INFORMATION:
37
38
               (A) NAME: Browdy, Roger L.
               (B) REGISTRATION NUMBER: 25,618
39
               (C) REFERENCE/DOCKET NUMBER: CAMPBELL=2A
40
41
42
        (ix) TELECOMMUNICATION INFORMATION:
43
               (A) TELEPHONE: (202) 628-5197
44
               (B) TELEFAX: (202) 737-3528
45
    (2) INFORMATION FOR SEQ ID NO:1:
46
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/804,166

DATE: 04/10/97 TIME: 17:05:30

	114FU1 5E1. 51065	iz.iuw
47 48 49 50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1049 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single 	
52 53	(D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
54 55 56 57	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 2781047	
58 59 60	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
61 62	TCCACATGGC TACAGGTAAG CGCCCCTAAA ATCCCTTTGG GCACAATGTG TCCTGAGGGG	60
63 64	AGAGGCAGCG ACCTGTAGAT GGGACGGGGG CACTAACCCT CAGGTTTGGG GCTTCTCAAT	120
65 66	CTCACTATCG CCATGTAAGC CCAGTATTTG GCCAATCTCA GAAAGCTCCT CCTCCCTGGA	180
67 68	GGGATGGAGA GAGAAAAACA AACAGCTCCT GGAGCAGGGA GAGTGCTGGC CTCTTGCTCT	240
69 70 71 72	CCGGCTCCCT CTGTTGCCCT CTGGTTTCTC CCCAGGC TCC CGG ACG TCC CTC Ser Arg Thr Ser Leu Leu 1 5	295
73 74 75 76	CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala 10 15 20	343
77 78 79 80	GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCC Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser 25 30 35	391
81 82 83 84	ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys 40 45 50	439
85 86 87 88	CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser 55 60 65 70	487
89 90 91 92	TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys 75 80 85	535
93 94 95 96	TGC CGA AAS GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp 90 95 100	583
97 98 99	CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp 105 110 115	631

RAW SEQUENCE LISTING PATENT APPLICATION US/08/804,166

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101 102						CAG Gln											679
102	Der	120	ASII	Беа	rne	0111	125	1110	ASII	Cys	501	130	O, D	пса	AD.	4 -7	
104																	
105	ACC	GTG	CAC	CTC	TCC	TGC	CAG	GAG	AAA	CAG	AAC	ACC	GTG	TGC	ACC	TGC	727
106	Thr	Val	His	Leu	Ser	Cys	Gln	Glu	Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	
107	135					140					145					150	
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109 110						CTA Leu											775
111	птъ	Ата	СТУ	Pne	155	Leu	Arg	GIU	ASII	160	Cys	Val	Ser	Cys	165	GIY	
112					100												
113	GCT	GCC	CCA	GGT	TGC	CCA	GAA	TGC	ACG	CTA	CAG	GAA	AAC	CCA	TTC	TTC	823
114	Ala	Ala	Pro	Gly	Cys	Pro	Glu	Cys	Thr	Leu	Gln	Glu	Asn	Pro	Phe	Phe	
115				170					175					180			
116																	
117						CCA											871
118 119	ser	GIN	185	GTÄ	АТА	Pro	тте	190	GIN	cys	мет	сту	195	cys	Pne	Ser	
120			103					190					1)3				
121	AGA	GCA	TAT	CCC	ACT	CCA	CTA	AGG	TCC	AAG	AAG	ACG	ATG	TTG	GTC	CAA	919
122						Pro											
123		200					205					210					
124																	
125						GAG											967
126 127	LуS 215	ASN	vaı	Thr	ser	Glu 220	ser	Thr	cys	Cys	225	АТА	гуѕ	Ser	туг	230	
128	213					220					223					230	
129	AGG	GTC	ACA	GTC	ATG	GGG	GGT	TTC	AAA	GTG	GAG	AAC	CAC	ACG	GGG	TGC	1015
130						Gly											
131					235					240					245		
132														*			
133						TAT					TA	AG					1049
134 135	HIS	cys	ser	250	Cys	Tyr	Tyr	HIS	255	Ser							
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140	(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO: 2	:								
141				~~~		a		- D T G		_							
142 143			(1):	_		CHAI GTH:											
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149 150		()	K1) :	SEQUI	ENCE	DESC	RIP	rion:	: SE(QI Ç	NO:2	:					
150	Ser	Ara	Thr	Ser	Leu	Leu	Leu	Δla	Phe	G] v	Leu	Leu	Cvs	Leu	Pro	Trp	
152	1	9			5					10			-]		15	F	

RAW SEQUENCE LISTING PATENT APPLICATION US/08/804,166

INPUT SET: S16859.raw

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153 154 155 156	Leu	Gln	Glu	Gly 20	Ser	Ala	Asp	Ser	Val 25	Cys	Pro	Gln	Gly	Lys 30	Tyr	Ile
157 158 159	His	Pro	Gln 35	Asn	Asn	Ser	Ile	Cys 40	Cys	Thr	Lys	Cys	His 45	Lys	Gly	Thr
160 161 162	Tyr	Leu 50	Tyr	Asn	Asp	Cys	Pro 55	Gly	Pro	Gly	Gln	Asp 60	Thr	Asp	Cys	Arg
163 164 165	Glu 65	Cys	Glu	Ser	Gly	Ser 70	Phe	Thr	Ala	Ser	Glu 75	Asn	His	Leu	Arg	His 80
166 167 168	_			_	85				Lys	90					95	
169 170 171	Ser	Ser	Cys	Thr 100	Val	Asp	Arg	Asp	Thr 105	Val	Cys	Gly	Cys	Arg 110	Lys	Asn
172 173 174		-	115		-	-		120	Asn				125			-
175 176 177		130				_	135		His			140				
178 179 180	145			_		150			Gly		155		_			160
181 182 183	-			-	165	_			Pro	170				_	175	
184 185 186				180					Pro 185	_				190		_
187 188 189		_	195					200	Tyr				205			
190 191 192	-	210					215		Val			220			_	_
193 194 195	225					230			Thr		235					240
196 197 198	Glu	Asn	His	Thr	Gly 245	Cys	His	Cys	Ser	Thr 250	Cys	Tyr	Tyr	His	Lys 255	Ser
199 200 201	(2)	INF	ORMA!	гіои	FOR	SEQ	ID 1	10 : 3	:				•	•		
202 203 204 205		(i)	() ()	A) LI 3) T	CE CH ENGTH YPE: TRANI	i: 12	202 k Leic	oase acio	pai:	cs		1	•			
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206	(D) TOPOLOGY: linear	
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208	(ii) MOLECULE TYPE: cDNA	
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210	(ix) FEATURE:	
211	(A) NAME/KEY: CDS	
212	(B) LOCATION: 2791199	
213		
214	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
215		
216	CTCGAGATGG CTACAGGTAA GCGCCCCTAA AATCCCTTTG GGCACAATGT GTCCTGAGGG	60
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223		
224	TCCGGCTCCC TCTGTTGCCC TGTGGTTTCT CCCCAGGC TCC CGG ACG TCC CTG	293
225	Ser Arg Thr Ser Leu	
226	260	
227		
228	CTC CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT	341
229	Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser	
230	265 270 275	
231		
232	GCC GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT	389
233	Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn	
234	280 285 290	
235	•	
236	TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC	437
237	Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp	
238	295 300 305	
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240	TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC	485
241	Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly	
242	310 315 320 325	
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244	TCT TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC	533
245	Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser	
246	330 335 340	
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248	AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG	581
249	Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val	
250	345 350 355	
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253	Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr	
254	360 365 → 370	
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257	Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn	
258	375 380 385	

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/08/804,166

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